AMENDMENTS TO THE CLAIMS

1. **(Currently amended)** A method for identifying and/or quantifying a biological organism in a sample by detecting a nucleotide sequence of said biological organism, wherein said nucleotide sequence presents a homology higher than 30% with ~~is homologous to~~ at least 4 other homologous nucleotide sequences from other biological organisms, comprising:

amplifying or copying at least one of said homologous nucleotide sequences into full-length double-stranded target homologous nucleotide sequences having between 100 and 800 bases using primer pairs which are capable of amplifying or copying at least four of said target homologous nucleotide sequences from other organisms;

contacting said full-length double-stranded target homologous nucleotide sequences resulting from the amplifying step with single-stranded different capture nucleotide sequences, at least two of said single-stranded capture nucleotide sequences being specific for at least two of said target homologous nucleotide sequences, said single-stranded capture nucleotide sequences being covalently bound in an array to an insoluble solid support via a spacer comprising a nucleotide sequence greater than 40 bases ~~which is at least 6.8 nm in length~~, said array comprising at least four different bound single-stranded capture nucleotide sequences/cm^2 of solid support surface, and wherein each of said single-stranded capture nucleotide sequences comprises a nucleotide sequence of about 5 to about 60 bases wherein said nucleotide sequence of about 5 to about 60 bases is able to specifically bind to one of the full-length target homologous nucleotide sequences without binding to said at least four other homologous nucleotide sequences, wherein said array also contains consensus capture nucleotide sequences for a common detection of said full-length target homologous nucleotide sequences, said consensus capture nucleotide sequences having a length specific of the target comprising between about 10 and about 1000 bases, and

detecting specific hybridization of the full-length target homologous nucleotide sequence to said single-stranded capture nucleotide sequences,

wherein said single-stranded capture nucleotide sequence is bound to the insoluble solid support at a specific location upon the array, and

wherein the binding between said full-length target homologous nucleotide sequence and its corresponding single-stranded capture nucleotide sequence forms a signal at the expected

location, the detection of said signal allowing a discrimination of the target homologous nucleotide sequence being specific of said organism from other organisms from the same or other groups, sub-groups or sub-sub-groups of said organisms.

2. **(Previously presented)** The method of claim 1, wherein said biological organism is present in the sample among at least 2 other organisms.

3. **(Previously presented)** The method of claim 1, wherein said biological organism is present in the sample among at least 4 other organisms.

4. **(Previously presented)** The method of claim 1, further comprising extracting the nucleotide sequence from said organism.

5. **(Previously presented)** The method of claim 1, further comprising labeling said organism or its nucleotide sequence as targets.

6. **(Original)** The method of claim 1, wherein said organism is a microorganism.

7. **(Currently amended)** The method of claim 1, further comprising identifying and/or quantifying the presence of several groups, sub-groups or sub-sub-groups of said organisms being related to each other, wherein the binding between full-length target homologous nucleotide sequences and corresponding consensus capture nucleotide sequences forms a signal at an expected location allowing the identification of a target nucleotide sequence specific of a group, sub-group or sub-sub-group of organisms.

8. **(Currently amended)** The method of claim 7, wherein the array contains two categories of capture nucleotide sequences, a first category of capture nucleotide sequences being specific for individual full-length target nucleotide sequences or their sub-groups and a second category of capture nucleotide sequences being specific for all the nucleotide sequences of the group.

9. **(Canceled)**

10. **(Canceled)**

11. **(Currently amended)** The method of claim 1, wherein said consensus capture nucleotide sequences has a sequence specific for the full-length target nucleotide sequences, said consensus capture nucleotide sequences comprising a sequence which is between about 100 and 600 bases in length.

12. **(Canceled)**

13. **(Currently amended)** The method of claim 1, wherein the amplified full-length target nucleotide sequence is a DNA nucleotide sequence amplified by PCR.

14. **(Currently amended)** The method of claim 1, wherein all or most of the full-length target amplified sequences are obtained by PCR with the same primer pair.

15. **(Currently amended)** The method of claim 1, wherein the presence of any full-length target amplified nucleotide sequence is firstly detected during the genetic amplification cycles and thereafter identified on the array.

16. **(Currently amended)** The method of claim 1, wherein the step of detecting the presence of any amplified full-length target nucleotide sequences and the genetic amplification step are performed in a same chamber.

17. **(Currently amended)** The method of claim 1, wherein the amplified full-length target nucleotide sequence is mRNA first reverse transcribed into cDNA and then amplified with the same primer pair which is capable of amplifying at least two of said homologous mRNA in said sample.

18. **(Currently amended)** The method of claim 1, wherein the homologous nucleotide sequences are copied by using the same primer pair.

19. **(Canceled)**

20. **(Currently amended)** The method of claim 1, wherein said spacer ~~is a nucleotide sequence of between about 15~~ greater than 40 and less than about 1000 bases.

21. **(Currently amended)** The method of claim 1, wherein spacer ~~is a nucleotide sequence of between about 30~~ greater than 40 and less than about 120 bases.

22. **(Canceled)**

23. **(Canceled)**

24. **(Canceled)**

25. **(Previously presented)** The method of claim 1, wherein the length of the specific sequence of the capture nucleotide sequence able to hybridize with the corresponding full-length target nucleotide sequences is comprised between about 20 and about 30 bases.

26. **(Previously presented)** The method of claim 1, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 10 fmoles per cm^2 of solid support surface.

27. **(Previously presented)** The method of claim 1, wherein the density of the capture nucleotide sequences bound to the solid support surface at a specific location is greater than 100 fmoles per cm^2 of solid support surface.

28. **(Canceled)**

29. **(Canceled)**

30. **(Currently amended)** The method of claim 1, wherein the ~~target~~ nucleotide sequence(s) to be detected present(s) a homology of greater than about 40% with other homologous nucleotide sequences.

31. **(Currently amended)** The method of claim 1, wherein the ~~target~~ nucleotide sequence(s) to be detected present(s) a homology of greater than about 60% with other homologous nucleotide sequences.

32. **(Currently amended)** The method of claim 1, wherein the ~~target~~ nucleotide sequence(s) to be detected present(s) a homology of greater than about 80% with other homologous nucleotide sequences.

33. **(Currently amended)** The method of claim 1, wherein the full-length target nucleotide sequences are labelled by a marker and wherein the signal resulting from hybridization by complementary bases pairing between the full-length target nucleotide sequence and its corresponding capture nucleotide sequence is obtained from the detection of said marker.

34. **(Canceled)**

35. **(Previously presented)** The method of claim 1, wherein other primers are present in the amplification step for the amplification of an antibiotic resistance determining nucleotide sequence.

36. **(Canceled)**

37. **(Canceled)**

38. **(Previously presented)** The method of claim 1, wherein the solid support comprises single-stranded capture nucleotide sequences specific for the identification of two or more *Staphylococcus* species, said solid support further comprises a consensus capture nucleotide sequence for a *Staphylococcus* genus identification.

39. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample differs from at least one of its homologous nucleotide sequences present in the sample by one or more base(s).

40. **(Currently amended)** The method of claim 1, wherein the arrays contain ~~contained~~ two to four single-stranded capture nucleotide sequences differing from each other by one or more base(s).

41. **(Cancelled)**

42. **(Cancelled)**

43. **(Cancelled)**

44. **(Original)** The method of claim 1, wherein the quantification of the organism present in the biological sample is obtained by the quantification of the signal.

45. **(Previously presented)** The method of claim 1, wherein the insoluble solid support is selected from the group consisting of glass, an electronic device, a silicon support, a plastic support, silica, metal and a mixture thereof, wherein said support is prepared in a format selected from the group consisting of slides, discs, gel layers and microbeads.

46. **(Previously presented)** The method of claim 6, wherein the microorganism to be identified and/or quantified in the sample belongs to the Staphylococci species selected from the group consisting of *S. aureus, S. epidermidis, S. saprophyticus, S. hominis* and *S. haemolyticus*.

47. **(Previously presented)** The method of claim 6, wherein the microorganism to be identified and/or quantified in the sample belong to the Mycobacteria genus.

48. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample is a sequence which belongs to the MAGE family.

49. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample is a sequence which belongs to the *HLA-A* family.

50. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample is a G protein-coupled receptor.

51. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample is a dopamine receptor.

52. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample is a choline receptor.

53. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample is a histamine receptor.

54. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified in the sample is a sequence which belongs the Cytochrome P450 isoforms family.

55. **(Previously presented)** The method of claim 6, wherein the microorganism to be identified and/or quantified in the sample belongs to a Gram-positive or Gram-negative family bacteria.

56. **(Original)** The method of claim 7, wherein the group, sub-group or individual targets correspond to families, genus, species, subtypes or individual organisms.

57. **(Original)** The method of claim 7, wherein the families, genus, species, subtypes or individuals are bacteria.

58. **(Previously presented)** The method of claim 57, wherein bacteria belongs to at least two of the genus families selected from the group consisting of *Staphylococcus*, *Enterococcus*, *Streptococcus*, *Haemolyticus*, *Pseudomonas*, *Campylobacter*, *Enterobacter*, *Neisseria*, *Proteus*, *Salmonella*, *Simonsiella*, *Riemerella*, *Escherichia*, *Neisseria*, *Meningococcus*, *Moraxella*, *Kingella*, *Chromobacterium* and *Branhamella*.

59. **(Previously presented)** The method of claim 1, wherein the identification of the nucleotide sequences allows an identification of the polymorphism of an organism.

60. **(Previously presented)** The method of claim 1, wherein the identification of the nucleotide sequences allows the genotyping of an organism.

61. **(Previously presented)** The method of claim 1, wherein the identification of the nucleotide sequences allows the identification of a single nucleotide polymorphism.

62.-80. **Canceled**

81. **(Previously presented)** The method of claim 1, wherein said single-stranded capture nucleotide sequences comprise a nucleotide sequence of between about 15 and about 40 bases, which is able to specifically bind to said target nucleotide sequence without binding to said at least four homologous nucleotide sequences from other organisms.

82. **(Cancelled)**

83. **(Cancelled)**

84. **(Previously presented)** The method of claim 1, wherein other primers are present in the amplification step for the amplification of another nucleotide sequence.

85. **(Previously presented)** The method of claim 1, wherein the nucleotide sequence to be identified and/or quantified is an RNA sequence submitted to a reverse transcription of its 3' or 5' end by using a consensus primer.

86. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be identified and/or quantified are from the *FemA* gene of Staphylococci species selected from the group consisting of *S. aureus*, *S. epidermidis*, *S. saprophyticus*, *S. hominis* and *S. haemolyticus*.

87. **(Previously presented)** The method of claim 1, wherein the solid support also bears another capture consensus nucleotide sequence able to bind to said full-length target nucleotide sequence and to said at least four homologous nucleotide sequences.

88. **(Cancelled)**

89. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be identified and/or quantified are from the gene encoding sub-unit A of gyrase.

90. **(Previously presented)** The method of claim 54, wherein the Cytochrome P450 isoforms family comprises a Cytochrome P450 2D6 and a 2C19 isoforms.

91. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be identified and/or quantified in the samples come from different animal species and genus belonging to families selected from the group consisting of: *Galinaceae*, *Leporidae*, *Suidae* and *Bovidae*.

92. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be detected and/or quantified in the samples belong to specific fishes species selected from the group consisting of *G. morhua, G. macrocephalus, P. flesus, M. merluccius, O. mykiss, P. platessa, P. virens, S. salar, S. pilchardus, A. thazard, T. alalunga, T. obesus, R. hippoglossoides, S. trutta, S. sarda, T. thynnus, S. scombrus* belonging to genera selected from the group consisting of: Auxis, Sarda, Scomber, Thunnus, Oncorhynch, Salmo, Merluccius, Pleuronectes, Platichtlys, Reinhardtius, Pollachius, Gadus, Sardina, from several families selected from the group consisting of: *Scombridae, Salmonidae, Merluccidae, Pleuronectidae, Gadidae* and *Clupeidae*.

93. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be detected and/or quantified in the samples belong to different plant species and genus

selected from the group consisting of Potato, tomato, oryza, zea, soja, wheat, barley, bean and carrot.

94. **(Previously presented)** The method of claim 1, wherein the nucleotide sequences to be detected and/or quantified in the samples are genetically modified organisms.

SUMMARY OF INTERVIEW

Exhibits and/or Demonstrations

None

Identification of Claims Discussed

Claims 1-8, 11-18, 20-23, 25-27, 29-36, 38-40, 44-61, 81, and 83-94

Identification of Prior Art Discussed

Guschin et al. (*Appl. Environ. Microbiol.* 1997 63:2397-2402)

Proposed Amendments

Proposed amending Claim 1 to specify that the target homologous nucleotide sequences resulting from the amplifying step are full-length, and that the spacer is a nucleic acid spacer.

Principal Arguments and Other Matters

The inventor, Nathalie Zammatteo, described the claimed invention, and compared its features to the methods of the prior art references. Guschin et al. does not use full-length amplified sequences as target. Guschin clones PCR amplicons of approximately 1,500 bases and then expresses labeled RNA. The labeled RNA fragmented to pieces of approximately 40 bp in length are applied to the support. Guschin does not use a nucleotide spacer on the microchip support. Therefore, the method of the present invention is quite different of the cited reference as it uses: short capture sequences (5-60 nucleotides), and requires direct labeling of the amplicons which are 100-800 bases long without prior fragmentation. Therefore, the cited references do not provide suggestion or motivation to modify the references to achieve the claimed invention, and do not teach or suggest all the claim limitations.

Results of Interview

The Examiner suggested that a submission of a 132 Declaration showing unexpected results using the claimed method may be helpful in overcoming any future references uncovered after Claim 1 has been amended.